To generate p(-3348/-150)*SCD*-luc (c1), clone 19 was digested with *Pst*I and *Sac*II and blunted with T4 polymerase. All sequences herein are numbered relative to the translation start site, designated +1. The 3.2 kb fragment containing only the 5' end of the gene was cloned into a blunted *Hin*dIII site of the luciferase vector pGL3-basic (Promega, Madison, WI, USA). p(-2328/-150)*SCD*-luc (c2) and p(-1295/-150)*SCD*-luc (c4) were generated by digesting the clone 19 with *Taq*I/*Sac*II and *Kpn*I/*Sac*II, respectively, and the resulting fragments were subcloned into a blunted *Hin*dIII site of pGL3-basic. p(-1537/-150)*SCD*-luc (c3) and p(-882/-150)*SCD*-luc (c5) were subsequently generated by digesting c1 with *Sac*I and *Sma*I, respectively. The resulting fragments were religated using T4 ligase. p(-461/-150)*SCD*-luc (c6) was generated by digesting c4 with *Eae*I/*Nco*I and the resulting fragment was ligated to blunted *Nco*I/*Hind*III sites of pGL3-basic. p(-270/-150)*SCD*-luc (c7) was created by digesting c4 with *Hinc*II and *Nco*I. The resulting fragment was subcloned into *Nco*I/*Hind*III digested, blunted, pGL-3 basic. p(-753/-150)*SCD*-luc (c8), p(-609/-150)*SCD*-luc (c9) and p(-496/-150)*SCD*-luc (c10) constructs were assembled by polymerase chain reaction using one of the three specific sense oligonucleotides (bp -753 to -732, c8), 5'-GGTTCACCACTGTTTCCTGAGA-3' (SEQ ID NO: 1); (-609 to -688, c9) 5'-GATGCCGGGCAGAGGCCCAGCG -3' (SEQ ID NO: 2);(–496 to -474, c10), 5'-GGCAACGGCAGGACGAGGTGGCA-3' (SEQ ID NO: 3); and a common antisense oligonucleotide (-166 to -145) 5'-CCGCGGTGCGTGGAGGTCCCCG-3' (SEQ ID NO: 4). All PCR reactions were conducted with proofreading Turbo *PFU* DNA polymerase (Stratagene, La Jolla, CA, USA), and the original c5 construct was used as template. Amplification products were phosphorylated with T4 kinase and subcloned into the *Hind*III blunted site of pGL-3 basic. The sequence of the PCR products were examined for accuracy using the dideoxynucleotide chain termination method.

a2

Please replace the paragraph beginning on page 14, line 8 with the following rewritten paragraph:

Total RNA was extracted from human hair follicle biopsies and cultured HaCaT keratinocytes (Boukamp *et al.*, 1988) using RNAzol (TEL-TEST Inc., Friendswood, TX, USA). A *SCD* fragment was amplified with PCR, using clone 19 as a template with the following primers: sense (-275 to -256), 5'GCCAGTCAACTCCTCGCACT3' (SEQ ID NO: 5); antisense (+7 to +27), 5'ATCGTCCTGCAGCAAGTGGGC3' (SEQ ID NO: 6). This

a3

resulted in a 302 bp fragment (nucleotide -275 to +27) which was subcloned into the TA cloning vector pCR2.1 (Invitrogen, Carlsbad, CA, USA). The plasmid (NPA1-pCR2.1) was further digested by Xba1 and EcoRV to release unnecessary vector sequence between the insert and the T7 promoter and religated with T4 ligase. The final construct (NPA2-pCR2.1) was linearized by H*ind*III and a labeled antisense RNA (400 bp) was synthesized from the T7 promoter of the plasmid using T7 RNA polymerase (Ambion, Austin, TX, USA). Following synthesis, the full-length probe was gel purified. Total RNA (15ug per sample) from human hair follicles and HaCaT keratinocytes was hybridized to the labeled transcript for 16h at 42°C. The RNA samples were digested with an RNase mixture (Ambion, Austin , TX, USA), and the sizes of the protected RNA were determined by electrophoresis on a 5% denaturing polyacrylamide gel, using a DNA sequencing ladder generated from NPA2-pCR2.1.

a3 cont

Please replace the paragraph beginning on page 14, line 29, with the following rewritten paragraph:

Nuclear extracts of HaCaT keratinocytes were prepared using standard procedures (Dignam *et al.*, 1983). Protein concentrations of the extract were determined with BCA assay (Pierce, Rockford, IL, USA). Electrophoretic mobility shift assays were performed with a Gel Shift assay system according to the manufacture's instruction (Promega, Madison, WI, USA). Briefly, hybridization was performed at room temperature for 20 min in a volume of 20 ul consisting of 0.1 pmol of probe (70, 000 cpm) and 5 ug of nuclear extract. The gel shift mixture was incubated for 20 min at room temperature, and samples were immediately electrophoresed at 150V for 3 h on a 5% nondenaturing acrylamide gel using 0.5 x TBE running buffer (34 mM Tris.borate, 0.75 mM EDTA ) prerun at 100 V for 100 min. The gel was then dried for autoradiography. For competition studies, radioinert DNA competitor was added as a 100-fold molar excess and preincubated with the nuclear extract at room temperature for 5 –10 min. The $^{32}$P-labeled DNA was then added to the mixture and incubated at room temperature. The oligonucleotides used for EMSAs were as follows: AP-2 (sense, -595 to –575), 5'-GCCCAGCGGCGGGTGGAAGAG-3' (SEQ ID NO: 7); AP-2 (antisense), 5'-CTCTTCCACCCGCCGCTGGGC-3' (SEQ ID NO: 8); SP-1 (sense, -559 to -539), 5'- AACAGAGGGGAGGGGGAGCGA-3' (SEQ ID NO: 9); SP-1(antisense), 5'-TCGCTCCCCCTCCCCTCTGTT-3' (SEQ ID NO: 10); CCAAT (sense, -509 to -484), 5'GCGCCGAGCCAATGGCAACGG-3' (SEQ ID NO: 11); CAAT (antisense), 5'-CCGTTGCCATTGGCTCGGCGC-3' (SEQ ID NO: 12).

a4

Please replace the paragraph beginning on page 16, line 8 with the following paragraph:

Mutation in the binding sites for transcription factors SP-1 and CCAAT were introduced into the plasmid *c9*, containing the 0.5 kb *SCD* promoter subcloned into the blunted HindIII site of pGL-3 basic, using the Quick Change Site-Directed Mutagenesis kit (Stratagene, La Jolla, CA, USA). Two double-stranded oligonuclotide primers containing the desired mutations are as follows (underlined base pairs denote mutant substitutions): 5'-AAGGAGAAACAGAGGAAAGGGGGAGCGAGGAGCTG-3' (SP-1) (SEQ ID NO: 13), and 5'-AGCAGATTGCGCCGAGAAAATGGCAACGGCAGGAC-3'(CCAAT) (SEQ ID NO: 14).

a5

Please amend Figures 1, 2, 5, and 8 as shown in the attached informal drawings.

a6.